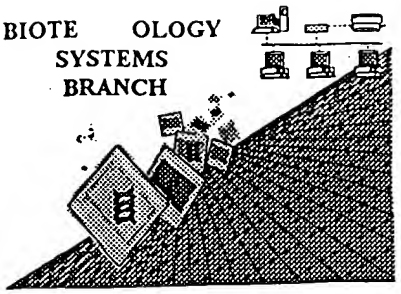
BIOTE OLOGY
SYSTEMS
BRANCH



0570
1005

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/881,572

Source: OIPE

Date Processed by STIC: 7/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/881,572

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2__J__	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3__J__	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4____	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5____	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7____	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8____	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10____	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11__J__	Use of <220>	Sequence(s) 20 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12____	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PATENT APPLICATION 601-1-095N
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT : Roth and Bupp

SERIAL NO. : to be assigned

FILED: June 14, 2001

FOR: TARGETING VIRAL VECTORS TO SPECIFIC CELLS

STATEMENT UNDER 37 CFR §1.821 and §1.825

Commissioner for Patents
Washington, D.C. 20231

S i r:

I hereby certify that:

_X_ The contents of the paper Sequence Listing and computer readable Sequence Listing submitted herewith are the same. (37 CFR §1.821(f)).

Respectfully submitted,

Attorney for applicant(s)
Catherine Roseman Smith
(Reg. No. 34240)
June 14, 2001

KLAUBER & JACKSON
411 Hackensack Avenue
Hackensack NJ 07601
Tel: (201) 487-5800

RE-RUN

OIPE

RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: US/09/881,572 TIME: 13:31:22

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07032001\I881572.raw

Does Not Comply
Corrected Diskette Needed

pp 1-4

3 <110> APPLICANT: Roth, Monica
5 Bupp, Keith.
7 <120> TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
9 <130> FILE REFERENCE: 601-1-095N
11 <140> CURRENT APPLICATION NUMBER: US/09/881,572
12 <141> CURRENT FILING DATE: 2001-06-14
14 <160> NUMBER OF SEQ ID NOS: 27
16 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
19 <211> LENGTH: 65
20 <212> TYPE: PRT
21 <213> ORGANISM: moloney murine leukemia virus
23 <400> SEQUENCE: 1
25 His Gly Pro Ser Tyr Trp Gly Leu Glu Tyr Gln Ser Pro Phe Ser Ser
26 1 5 10 15
28 Pro Pro Gly Pro Pro Cys Cys Ser Gly Gly Ser Ser Pro Gly Cys Ser
29 20 25 30
31 Arg Asp Cys Glu Glu Pro Leu Thr Ser Leu Thr Pro Arg Cys Asn Thr
E--> 32 35 40 ~~45~~ 45
34 Ala Trp Asn Arg Leu Lys Leu Asp Gln Thr Thr His Lys Ser Asn Glu
E--> 35 50 55 ~~60~~ 60
37 Gly
38 65

misaligned nos.
(see Item 3 on
Error Summary Sheet)

<210> SEQ ID NO: 11
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Rat Leukemia Virus
<400> SEQUENCE: 11
Gly Lys Arg Thr Arg Glu
1 5
<210> SEQ ID NO: 12
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Feline Leukemia Virus
<400> SEQUENCE: 12
Trp Glu Pro Ile Val Leu Asp Pro Thr Asn Val Lys His Gly Ala Arg
1 5 10 15
Tyr Pro Ser Ser Lys Tyr Gly Cys
20
<210> SEQ ID NO: 13
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Feline Leukemia Virus
<400> SEQUENCE: 13
Trp Glu Pro Met Ala Pro Asp Pro Arg Ser Trp Ala Arg Tyr Ser Ser
1 5 10 15
Ser Ile His Gly Cys
20
<210> SEQ ID NO: 14
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus Sequence
<220> FEATURE:
<221> NAME/KEY: X
<222> LOCATION: (9)..(13) (10)..(14)
<223> OTHER INFORMATION: X can be any amino acid. Xaa
<220> FEATURE:
<221> NAME/KEY: X
<222> LOCATION: (3)..(7) (4)..(8)
<223> OTHER INFORMATION: X is any amino acid.
<400> SEQUENCE: 14 Xaa
Trp Glu Pro Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Ser Ser
1 5 10 15
Ser Lys Tyr Gly Cys
20
<210> SEQ ID NO: 15
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Amphotropic Murine Leukemia Virus
<400> SEQUENCE: 15

RAW SEQUENCE LISTING DATE: 07/24/2001
PATENT APPLICATION: US/09/881,572 TIME: 09:35:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07242001\I881572.raw

214 Glu Glu Trp Asp Pro Ser Asp Gln Glu Pro Tyr Val Gly Tyr
215 1 5 10
217 <210> SEQ ID NO: 16
218 <211> LENGTH: 13
219 <212> TYPE: PRT
220 <213> ORGANISM: Amphotropic Murine Leukemia Virus
222 <400> SEQUENCE: 16
224 Pro Trp Asp Thr Gly Cys Ser Lys Val Ala Cys Gly Pro
225 1 5 10
227 <210> SEQ ID NO: 17
228 <211> LENGTH: 29
229 <212> TYPE: PRT
230 <213> ORGANISM: Amphotropic Murine Leukemia Virus
232 <400> SEQUENCE: 17
234 Val Gly Asp Thr Trp Glu Pro Ile Val Leu Asn Pro Thr Asn Val Lys
235 1 5 10 15
237 His Gly Ala Arg Tyr Ser Ser Ser Lys Tyr Gly Cys Lys
238 20 25
240 <210> SEQ ID NO: 18
241 <211> LENGTH: 26
242 <212> TYPE: PRT
243 <213> ORGANISM: Feline Leukemia Virus
245 <400> SEQUENCE: 18
247 Val Gly Thr Asp Trp Glu Pro Met Ala Pro Asp Pro Arg Ser Trp Ala
248 1 5 10 15
250 Arg Tyr Ser Ser Ser Thr His Gly Cys Lys
251 20 25
253 <210> SEQ ID NO: 19
254 <211> LENGTH: 19
255 <212> TYPE: PRT
256 <213> ORGANISM: Feline Leukemia Virus
258 <400> SEQUENCE: 19
260 Val Gly Glu Glu Trp Asp Pro Ser Asp Gln Glu Pro Tyr Val Gly Tyr
261 1 5 10 15
263 Gly Cys Lys
266 <210> SEQ ID NO: 20
267 <211> LENGTH: 72
268 <212> TYPE: DNA
Ok--> 269 <213> ORGANISM: Artificial
271 <220> FEATURE:
272 <223> OTHER INFORMATION: n is any nucleotide.
274 <220> FEATURE:
W--> 275 <221> NAME/KEY: N
276 <222> LOCATION: (22)..(36)
277 <223> OTHER INFORMATION: N is any nucleotide.
279 <220> FEATURE:
W--> 280 <221> NAME/KEY: N
281 <222> LOCATION: (39)..(53)
282 <223> OTHER INFORMATION: N is any nucleotide.

See Item 11 on Error Summary Sheet

(40)..(54)

```
     284 <400> SEQUENCE: 20
W--> 285 gtgggagaca cctgggaacc tnnnnnnnnn nnnnnnagan nnnnnnnnnn nnnntcctcc  60
     287 tcaaaatatg ga          72
     290 <210> SEQ ID NO: 21
     291 <211> LENGTH: 17
     292 <212> TYPE: DNA
     293 <213> ORGANISM: Feline Leukemia Virus
     295 <400> SEQUENCE: 21
     296 ctctgtggac ccttgga        17
     299 <210> SEQ ID NO: 22
     300 <211> LENGTH: 22
     301 <212> TYPE: DNA
     302 <213> ORGANISM: Feline Leukemia Virus
     304 <400> SEQUENCE: 22
     305 aggaggagtt ttatacctac at       22
     308 <210> SEQ ID NO: 23
     309 <211> LENGTH: 25
     310 <212> TYPE: PRT
     311 <213> ORGANISM: Homo sapiens POSSOBLY MODIFY
W--> 312 <220> FEATURE:
W--> 313 <221> NAME/KEY: X
     314 <222> LOCATION: (4)..(6)
     315 <223> OTHER INFORMATION: (X) is any amino acid.
W--> 317 <220> FEATURE:                Xaa
W--> 318 <221> NAME/KEY: X
     319 <222> LOCATION: (17)..(19)
     320 <223> OTHER INFORMATION: (X) is any amino acid.
     322 <400> SEQUENCE: 23                Xaa
W--> 324 Trp Glu Pro Xaa Xaa Xaa Ser Pro Tyr Ser Ser Asp Thr Thr Pro Ala
     325 1               5                  10                  15
W--> 327 Xaa Xaa Xaa Ser Ser Lys Tyr Gly Cys
     328             20                  25
     330 <210> SEQ ID NO: 24
     331 <211> LENGTH: 25
     332 <212> TYPE: PRT
     333 <213> ORGANISM: Amphotropic Murine Leukemia Virus
     335 <400> SEQUENCE: 24
     337 Glu Glu Trp Asp Pro Ser Asp Gln Glu Pro Tyr Val Gly Tyr Gly Cys
     338 1               5                  10                  15
     340 Lys Tyr Pro Ala Gly Arg Gln Arg Thr
     341             20                  25
     343 <210> SEQ ID NO: 25
     344 <211> LENGTH: 29
     345 <212> TYPE: PRT
     346 <213> ORGANISM: Amphotropic Murine Leukemia Virus
     348 <400> SEQUENCE: 25
     350 Pro Trp Asp Thr Gly Cys Ser Lys Val Ala Cys Gly Pro Cys Tyr Asp
     351 1               5                  10                  15
     353 Leu Ser Lys Val Ser Asn Ser Phe Gln Gly Ala Thr Arg
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 07/24/2001
PATENT APPLICATION: US/09/881,572 TIME: 09:35:18

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07242001\I881572.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:184 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:190 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:269 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:312 M:283 W: Missing Blank Line separator, <220> field identifier
L:313 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

VERIFICATION SUMMARY DATE: 07/05/2001
PATENT APPLICATION: US/09/881,572 TIME: 13:31:23

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07032001\I881572.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:184 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:190 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:269 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:312 M:283 W: Missing Blank Line separator, <220> field identifier
L:313 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23